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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/988,200

DATE: 01/26/2002  
TIME: 14:03:42

Input Set : N:\Crf3\RULE60\09988200.raw  
Output Set: N:\CRF3\01252002\I988200.raw

#### SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: BARBEYRON, Tristan  
6 POTIN, Philippe  
7 RICHARD, Christophe  
8 HENRISSAT, Bernard  
9 YVIN, Jean-Claude  
10 KLOAREG, Bernard

13 (ii) TITLE OF INVENTION: Glycolyse hydrolase genes and their  
14 use for producing enzymes for the biodegradation of  
15 carrageenans

17 (iii) NUMBER OF SEQUENCES: 8

19 (iv) CORRESPONDENCE ADDRESS:

21 (A) ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ  
22 (B) STREET: 612 Crystal Square 4, 1745 Jefferson Davis  
Highway  
23 (C) CITY: ARLINGTON  
24 (D) STATE: VIRGINIA  
25 (E) COUNTRY: U.S.A.  
26 (F) ZIP: 22202

28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk  
30 (B) COMPUTER: IBM PC compatible  
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

**ENTERED**

34 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/09/988,200  
C--> 36 (B) FILING DATE: 19-Nov-2001

37 (C) CLASSIFICATION:

43 (vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: 09/269,731  
41 (B) FILING DATE:  
44 (A) APPLICATION NUMBER: FR 96 12204  
45 (B) FILING DATE: 07-OCT-1996

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: IRA SCHULTZ  
49 (B) REGISTRATION NUMBER:  
50 (C) REFERENCE/DOCKET NUMBER:

52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: (703) 412-1155  
54 (B) TELEFAX: (703) 412-1161

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

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59 (A) LENGTH: 2085 base pairs  
 60 (B) TYPE: nucleic acid  
 61 (C) STRANDEDNESS: single  
 62 (D) TOPOLOGY: linear  
 64 (ii) MOLECULE TYPE: DNA (genomic)  
 66 (iii) HYPOTHETICAL: NO  
 70 (ix) FEATURE:  
 71 (A) NAME/KEY: CDS  
 72 (B) LOCATION:join(211..1683, 1880..2083)  
 74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 76 AAGCTTTCCG ATTCTATCAT CGAAGTCATA GGAGTGGTA AACAAAAAAAG CATGAAACTA 60  
 77 GCTTTTAAA ATACAGACTT TCAATATAGG TCGCACACAA TATTAACGAA TAAATAAGCA 120  
 78 AATCATATAC ATAATCATTG CTTTAAATAT GTTTTAAATAC AGATATAAAC ATAGTATGTT 180  
 79 TGTGTTTTG GTATCTATCG GAGTGAAAAC ATG CGC TTA TAT TTT AGA AAG TTG 234  
 80 Met Arg Leu Tyr Phe Arg Lys Leu  
 81 1 5  
 83 TGG TTA ACA AAT TTA TTT TTA GGC GGA GCA CTG GCC TCT TCA GCT GCG 282  
 84 Trp Leu Thr Asn Leu Phe Leu Gly Gly Ala Leu Ala Ser Ser Ala Ala  
 85 10 15 20  
 87 ATA GGG GCT GTC TCC CCC AAG ACT TAT AAG GAC GCA GAT TTT TAT GTT 330  
 88 Ile Gly Ala Val Ser Pro Lys Thr Tyr Lys Asp Ala Asp Phe Tyr Val  
 89 25 30 35 40  
 91 GCC CCT ACT CAA CAA GAT GTT AAC TAT GAT TTA GTT GAT GAT TTT GGC 378  
 92 Ala Pro Thr Gln Gln Asp Val Asn Tyr Asp Leu Val Asp Asp Phe Gly  
 93 45 50 55  
 95 GCT AAT GGA AAC GAC ACT AGT GAT GAC AGT AAT GCT TTA CAA AGA GCA 426  
 96 Ala Asn Gly Asn Asp Thr Ser Asp Asp Ser Asn Ala Leu Gln Arg Ala  
 97 60 65 70  
 99 ATT AAT GCT ATT AGT AGA AAA CCG AAT GGG GGC ACT TTA CTA ATA CCG 474  
 100 Ile Asn Ala Ile Ser Arg Lys Pro Asn Gly Gly Thr Leu Leu Ile Pro  
 101 75 80 85  
 103 AAT GGA ACT TAC CAT TTC CTC GGC ATA CAG ATG AAG TCG AAC GTA CAC 522  
 104 Asn Gly Thr Tyr His Phe Leu Gly Ile Gln Met Lys Ser Asn Val His  
 105 90 95 100  
 107 ATC CGT GTT GAG AGT GAC GTG ATA ATC AAG CCA ACG TGG AAT GGG GAT 570  
 108 Ile Arg Val Glu Ser Asp Val Ile Ile Lys Pro Thr Trp Asn Gly Asp  
 109 105 110 115 120  
 111 GGC AAA AAC CAC CGA CTA TTT GAA GTT GGC GTA AAC AAT ATT GTA AGA 618  
 112 Gly Lys Asn His Arg Leu Phe Glu Val Gly Val Asn Asn Ile Val Arg  
 113 125 130 135  
 115 AAC TTC AGC TTT CAA GGG TTA GGA AAC GGT TTT TTG GTG GAT TTT AAA 666  
 116 Asn Phe Ser Phe Gln Gly Leu Gly Asn Gly Phe Leu Val Asp Phe Lys  
 117 140 145 150  
 119 GAT TCT CGC GAC AAA AAC TTA GCT GTT TTT AAG TTA GGC GAT GTT AGA  
 120 Asp Ser Arg Asp Lys Asn Leu Ala Val Phe Lys Leu Gly Asp Val Arg  
 121 155 160 165  
 123 AAT TAC AAA ATT TCC AAT TTT ACC ATT GAT GAT AAT AAA ACG ATA TTT 762  
 124 Asn Tyr Lys Ile Ser Asn Phe Thr Ile Asp Asp Asn Lys Thr Ile Phe  
 125 170 175 180

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127	GCC TCA ATT TTA GTG GAC GTA ACA GAA CGT AAT GGG CGG TTA CAT TGG	810
128	Ala Ser Ile Leu Val Asp Val Thr Glu Arg Asn Gly Arg Leu His Trp	
129	185 190 195 200	
131	TCG CGT AAT GGA ATT ATC GAA AGA ATA AAA CAA AAT AAC GCT TTG TTC	858
132	Ser Arg Asn Gly Ile Ile Glu Arg Ile Lys Gln Asn Asn Ala Leu Phe	
133	205 210 215	
135	GGC TAC GGC CTT ATT CAA ACC TAT GGC GCA GAT AAT ATT TTG TTT AGG	906
136	Gly Tyr Gly Leu Ile Gln Thr Tyr Gly Ala Asp Asn Ile Leu Phe Arg	
137	220 225 230	
139	AAC CTC CAT TCG GAA GGC GGA ATT GCG TTA CGG ATG GAA ACT GAC AAC	954
140	Asn Leu His Ser Glu Gly Gly Ile Ala Leu Arg Met Glu Thr Asp Asn	
141	235 240 245	
143	TTA CTT ATG AAA AAT TAT AAG CAA GGC GGA ATA AGA AAC ATC TTT GCT	1002
144	Leu Leu Met Lys Asn Tyr Lys Gln Gly Gly Ile Arg Asn Ile Phe Ala	
145	250 255 260	
147	GAT AAT ATC AGA TGT AGC AAA GGA CTT CGC GCG GTC ATG TTT GGC CCA	1050
148	Asp Asn Ile Arg Cys Ser Lys Gly Leu Ala Ala Val Met Phe Gly Pro	
149	265 270 275 280	
151	CAT TTT ATG AAG AAT GGA GAT GTG CAA GTG ACC AAT GTC AGC TCA GTT	1098
152	His Phe Met Lys Asn Gly Asp Val Gln Val Thr Asn Val Ser Ser Val	
153	285 290 295	
155	AGT TGC GGT TCG GCT GTA CGA AGT GAT AGT GGA TTT GTC GAA CTC TTT	1146
156	Ser Cys Gly Ser Ala Val Arg Ser Asp Ser Gly Phe Val Glu Leu Phe	
157	300 305 310	
159	AGC CCG ACA GAC GAA GTA CAT ACG CGT CAA AGT TGG AAA CAA GCC GTT	1194
160	Ser Pro Thr Asp Glu Val His Thr Arg Gln Ser Trp Lys Gln Ala Val	
161	315 320 325	
163	GAA AGT AAA TTG GGC CGA GGG TGT GCG CAA ACC CCT TAT GCT AGA GGT	1242
164	Glu Ser Lys Leu Gly Arg Gly Cys Ala Gln Thr Pro Tyr Ala Arg Gly	
165	330 335 340	
168	AAT GGT GGT ACA CGG TGG GCG GCT CGC GTA ACA CAA AAA GAC GCG TGT	1290
169	Asn Gly Gly Thr Arg Trp Ala Ala Arg Val Thr Gln Lys Asp Ala Cys	
170	345 350 355 360	
172	TTA GAT AAA GCA AAA CTG GAA TAT GGA ATA GAG CCT GGT TCA TTT GGC	1338
173	Leu Asp Lys Ala Lys Leu Glu Tyr Gly Ile Glu Pro Gly Ser Phe Gly	
174	365 370 375	
176	ACG GTT AAA GTC TTT GAT GTT ACA GCG CGT TTT GGT TAT AAC GCA GAT	1386
177	Thr Val Lys Val Phe Asp Val Thr Ala Arg Phe Gly Tyr Asn Ala Asp	
178	380 385 390	
180	CTT AAA CAG GAC CAG CTA GAC TAC TTT TCT ACA TCC AAC CCT ATG TGC	1434
181	Leu Lys Gln Asp Gln Leu Asp Tyr Phe Ser Thr Ser Asn Pro Met Cys	
182	395 400 405	
184	AAG CGT GTC TGC CTT CCT ACA AAA GAA CAA TGG AGT AAG CAA GGC CAA	1482
185	Lys Arg Val Cys Leu Pro Thr Lys Glu Gln Trp Ser Lys Gln Gly Gln	
186	410 415 420	
188	ATT TAC ATT GGT CCG TCA TTA GCT GCA GTA ATT GAT ACC ACA CCT GAA	1530
189	Ile Tyr Ile Gly Pro Ser Leu Ala Ala Val Ile Asp Thr Thr Pro Glu	
190	425 430 435 440	
192	ACT TCA AAA TAC GAT TAT GAT GTG AAA ACT TTT AAC GTC AAA AGA ATA	1578

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193	Thr Ser Lys Tyr Asp Tyr Asp Val Lys Thr Phe Asn Val Lys Arg Ile			
194	445	450	455	
196	AAT TTT CCT GTA AAT TCA CAC AAG ACT ATC GAC ACG AAT ACT GAA AGT			1626
197	Asn Phe Pro Val Asn Ser His Lys Thr Ile Asp Thr Asn Thr Glu Ser			
198	460	465	470	
200	AGC CGT GTC TGC AAT TAT TAC GGT ATG TCC GAA TGC TCC AGC AGT CGA			1674
201	Ser Arg Val Cys Asn Tyr Tyr Gly Met Ser Glu Cys Ser Ser Arg			
202	475	480	485	
204	TGG GAG CGA TAGATTAAGC CGCTATATTG ATTTACTAGG TAAAACCTCA			1723
205	Trp Glu Arg			
206	490			
208	AGCCGCATTC GAAGAACTAT CGAACGCGGC TTTTTGTTA AGAGCGCTA TGACTCAGTA			1783
209	TATTTTGAT AAATATAATT TTACATCTG TTAAAGTAAA CATCATATGT TTATATAGGT			1843
210	GCAATCTAAT TTGTTAATAT AGTGTGGAG ATAGGT ATG AAA GGT GTT TCT ACG			1897
211	Met Lys Gly Val Ser Thr			
212	495			
215	AAA AAT GCT CTT TTA TTT GCA GGC TTT TCG TTA AGT CTA GTT GCA CAG			1945
216	Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala Gln			
217	500	505	510	
219	TCA GTT AGT GCA CAA GAA GCA AAA CAG CCT GAA AAA GAA GAA AAA GAT			1993
220	Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys Asp			
221	515	520	525	
223	GTT GAG GTG ATT TTG GTA TCG GCA CAA AAG CGT GAG CAA GCG CTT AAA			2041
224	Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu Lys			
225	530	535	540	545
227	GAA GTG CCT GTA TCA ATT GAA GTT ATT CAA GGC GAC CTT CTA GA			2085
228	Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu			
229	550	555		

232 (2) INFORMATION FOR SEQ ID NO: 2:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 559 amino acids

236 (B) TYPE: amino acid

237 (D) TOPOLOGY: linear

239 (ii) MOLECULE TYPE: protein

241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

243	Met Arg Leu Tyr Phe Arg Lys Leu Tip Leu Thr Asn Leu Phe Leu Gly			
244	1	5	10	15
245	Gly Ala Leu Ala Ser Ser Ala Ala Ile Gly Ala Val Ser Pro Lys Thr			
246	20	25	30	
247	Tyr Lys Asp Ala Asp Phe Tyr Val Ala Pro Thr Gln Gln Asp Val Asn			
248	35	40	45	
249	Tyr Asp Leu Val Asp Asp Phe Gly Ala Asn Gly Asn Asp Thr Ser Asp			
250	50	55	60	
251	Asp Ser Asn Ala Leu Gln Arg Ala Ile Asn Ala Ile Ser Arg Lys Pro			
252	65	70	75	80
253	Asn Gly Gly Thr Leu Leu Ile Pro Asn Gly Thr Tyr His Phe Leu Gly			
254	85	90	95	
255	Ile Gln Met Lys Ser Asn Val His Ile Arg Val Glu Ser Asp Val Ile			
256	100	105	110	

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257 Ile Lys Pro Thr Trp Asn Gly Asp Gly Lys Asn His Arg Leu Phe Glu  
 258 115 120 125  
 259 Val Gly Val Asn Asn Ile Val Arg Asn Phe Ser Phe Gln Gly Leu Gly  
 260 130 135 140  
 263 Asn Gly Phe Leu Val Asp Phe Lys Asp Ser Arg Asp Lys Asn Leu Ala  
 264 145 150 155 160  
 265 Val Phe Lys Leu Gly Asp Val Arg Asn Tyr Lys Ile Ser Asn Phe Thr  
 266 165 170 175  
 267 Ile Asp Asp Asn Lys Thr Ile Phe Ala Ser Ile Leu Val Asp Val Thr  
 268 180 185 190  
 269 Glu Arg Asn Gly Arg Leu His Trp Ser Arg Asn Gly Ile Ile Glu Arg  
 270 195 200 205  
 271 Ile Lys Gln Asn Asn Ala Leu Phe Gly Tyr Gly Leu Ile Gln Thr Tyr  
 272 210 215 220  
 273 Gly Ala Asp Asn Ile Leu Phe Arg Asn Leu His Ser Glu Gly Gly Ile  
 274 225 230 235 240  
 275 Ala Leu Arg Met Glu Thr Asp Asn Leu Leu Met Lys Asn Tyr Lys Gln  
 276 245 250 255  
 277 Gly Gly Ile Arg Asn Ile Phe Ala Asp Asn Ile Arg Cys Ser Lys Gly  
 278 260 265 270  
 279 Leu Ala Ala Val Met Phe Gly Pro His Phe Met Lys Asn Gly Asp Val  
 280 275 280 285  
 281 Gln Val Thr Asn Val Ser Ser Val Ser Cys Gly Ser Ala Val Arg Ser  
 282 290 295 300  
 283 Asp Ser Gly Phe Val Glu Leu Phe Ser Pro Thr Asp Glu Val His Thr  
 284 305 310 315 320  
 285 Arg Gln Ser Trp Lys Gln Ala Val Glu Ser Lys Leu Gly Arg Gly Cys  
 286 325 330 335  
 287 Ala Gln Thr Pro Tyr Ala Arg Gly Asn Gly Gly Thr Arg Trp Ala Ala  
 288 340 345 350  
 289 Arg Val Thr Gln Lys Asp Ala Cys Leu Asp Lys Ala Lys Leu Glu Tyr  
 290 355 360 365  
 291 Gly Ile Glu Pro Gly Ser Phe Gly Thr Val Lys Val Phe Asp Val Thr  
 292 370 375 380  
 293 Ala Arg Phe Gly Tyr Asn Ala Asp Leu Lys Gln Asp Gln Leu Asp Tyr  
 294 385 390 395 400  
 295 Phe Ser Thr Ser Asn Pro Met Cys Lys Arg Val Cys Leu Pro Thr Lys  
 296 405 410 415  
 297 Glu Gln Trp Ser Lys Gln Gly Gln Ile Tyr Ile Gly Pro Ser Leu Ala  
 298 420 425 430  
 299 Ala Val Ile Asp Thr Thr Pro Glu Thr Ser Lys Tyr Asp Tyr Asp Val  
 300 435 440 445  
 301 Lys Thr Phe Asn Val Lys Arg Ile Asn Phe Pro Val Asn Ser His Lys  
 302 450 455 460  
 303 Thr Ile Asp Thr Asn Thr Glu Ser Ser Arg Val Cys Asn Tyr Tyr Gly  
 304 465 470 475 480  
 305 Met Ser Glu Cys Ser Ser Ser Arg Trp Glu Arg Met Lys Gly Val Ser  
 306 485 490 495  
 307 Thr Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/988,200

DATE: 01/26/2002  
TIME: 14:03:43

Input Set : N:\Crf3\RULE60\09988200.raw  
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L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]